

## Oral Health Status: The Level of Oral Microbial Flora in Healthy Girls

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### ABSTRACT

The normal oral flora comprises a diverse group of micro-organisms and then 300 species inhabit the oral cavity of which about 50 are found routinely and account for the majority of the cultivable strains, these factors, together with the fact that the indigenous microbiota plays an important role in health and disease of a human and animals. It contribute to the development of the immune system and provide resistance to colonization by allochthonous or pathogenic micro-organisms. The aim of our study is to determine the most frequent micro-organisms as normal flora in healthy individuals. A total of 30 healthy students, all belongs to Jinnah University for Women of same age group were studied. Throat swabs were plated with human-blood agar, chocolate agar and apply bacitracin disk on both plates, SDA agar were incubating for 24 hours for isolation of *Candida species*. Organisms were cultured on Blood agar, SDA agar, Mannitol salt agar to observe the colonies. Different spot test like catalase and coagulase test were performed for identification of *Staphylococcus species*. Identification was also done by microscopic examination by gram stain. Catalase-positive, gram-positive rods were found to be as most frequent micro-organisms as normal flora of healthy students and were only micro-organisms detected 46.6% and total *Staphylococcus species* were (30%); *Staphylococcus aureus* (13%) and other *Staphylococcus species* (17 %) where as *Streptococcus species* (catalase -negative gram positive cocci) isolated from oral specimen of healthy individuals.

**Key words:** Microbiota, Oral flora, *Staphylococcus sp.*, Throat swab.

### INTRODUCTION

The microbial flora of the oral cavity are rich and extremely diverse. This reflects the abundant nutrients and moisture and hospitable temperature, and the availability of surface on which bacterial populations can develop. The presence of a myriad of micro-organisms is a natural part of proper oral health. However, an imbalance in the microbial flora can lead to the production of acidic compounds by some micro-organisms that can damage the teeth and gums. Damage to the teeth is referred to a dental caries. It has been estimated that at least 35% of dentate U.S adults aged 30 to 90 years have Peridontitis

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(Yamamoto *et al.*, 1994). In addition specific oral bacterial species have been implicated several systemic disease, such as bacterial endocarditis (Michalek *et al.*, 1990) aspiration pneumonia (Childers *et al.*, 1989), osteomyelitis in children (Farnaud *et al.*, 2003) preterm low birth weight (Corthesy *et al.*, 1999) and cardiovascular disease (Tenovuo *et al.*, 1994). Surprisingly, little known about the microflora of the healthy oral cavity. These include the tongue, epithelial cells lining the roof of the mouth and the cheeks, the hard enamel of the teeth. In particular, the microbial communities that exist on the surface of the teeth are known as dental plaque. The adherent communities also represent a biofilm. Oral biofilm develop over it time into

exceedingly complex communities. Hundreds of species of bacteria have been identified in such biofilm. Examples of some bacteria that are typically present as primary colonizers include Streptococcus, Actinomycetes, Neisseria and Veillonella. Example of secondary colonizers include *Fusobacterium nucleatum*, *Prevotella intermedia* and *Capnocytophaga species*. With further time, another group of bacteria can become associated with the adherent community. Examples of these bacteria include *Campylobacter rectus*, *Eikenella corrodens*, *Actinobacillus Actinomycetem comitans*, and the oral spirocheates of the genus *Treponema*. The mouth is the largest natural opening in the human body, and is a major component in the mucosal barrier system. It has its own immune barriers, which we call the oral immune system. The primary function of the immune system of the mouth is to protect the teeth, jaws, gingivae and the rest of the oral mucosa against infection (Yamamoto *et al.*, 1994). The flow of saliva has a mechanical effect, flushing microorganism from mucosal and tooth surfaces. Saliva also contains important antimicrobial agents (Tenovuo *et al.*, 1994). The intact stratified squamous epithelium supported by the lamina propria presents a mechanical barrier to oral microorganism. The continuous shedding by exfoliation of epithelial squamous limits microbial colonization of the surface. Intra-epithelial dendritic langerhans cells are peripheral antigen-presenting cells which can process antigen in their MHC-class II abundant intracellular compartments. They migrate to the regional lymph nodes to present antigenic peptides complexed to MHC-class II molecules to prime naïve helper T cells. The oral epithelium also forms part of an intercommunicating network of the immune system, in which signals are regularly exchanged in dynamic interactions (Yamamoto *et al.*, al 1994) as the nonspecific defense factors include mucins, nonimmune salivary glycoproteins, lactoferrin, lysozyme, peroxidase, histatins, and cystatins. SIgA is considered the first line of defense against pathogens which colonize and invade surfaces bathed by secretions (Mcnabb *et al.*, 1981). SIgA antibodies may play an important role in the homeostasis of

oral resident microbiota and in the prevention against caries and periodontal diseases (Michalek *et al.*, 1990). The normal oral flora comprises a diverse group of micro-organism, including bacteria, fungi, protozoa and possibly even viruses (Marsh *et al.*, 1999). More than 300 species inhabit the oral cavity of which about 30 are found routinely and account for the majority of the cultivable strains, these factors, together with the fact that the oral cavity has a wide range of sites with different environment condition, make the study of oral microbiology complex and difficult. The indigenous microbiota plays an important role in health and disease of humans and animals. It contributes to the development of the immune system and provides resistance to colonization by allochthonous or pathogenic micro-organisms (Crabbe *et al.*, 1968).

## MATERIALS AND METHODS

*Specimen:* A sterile cotton swab specimen, vigorously rub on both tonsillar surface and the posterior pharynx. Remove swab from mouth and insert tip down into wrapper.

*Requirements:* Petri plates, sterile cotton swabs, test tubes, pipettes.

*Media and Reagents:* Catalase reagent, Blood base, Mannitol salt agar, bacitracin disk, gram staining reagents.

*Procedure:* Throat swabs were plated with human-blood agar, and SDA agar. Place bacitracin disk on blood agar plates. Both plates were incubated at 37 °C for 24 hours. Gram staining was performed to observe the gram reaction and morphology of micro-organism. The organisms were streaked in order to check haemolysis. Catalase test and coagulase test were also performed.

## RESULTS

Catalase-positive, Gram-positive rods were found to be as most frequent micro-organisms as normal

flora of healthy students and were only micro-organisms detected 46.6% and total gram positive cocci were found 53% in which total *Staphylococcus species* were 30%; *Staphylococcus aureus* 13% while other *Staphylococcus species* were 17 % where as catalase-negative Gram-positive cocci were also isolated from oral specimen of healthy individuals (Table I).

**Table I.** Frequency rate of isolated micro-organisms from oral cavity.

Microorganisms	No. of Individuals	Percentage (%)
<i>Staphylococcus aureus</i>	4	13
Other <i>Staphylococcus species</i>	5	17
Catalase positive, gram-positive rods	14	47
Catalase-negative gram-positive cocci	7	23
Candida	0	0

### DISCUSSION AND CONCLUSION

There is a distinctive bacterial flora in the healthy oral cavity which is different from that of oral disease for example, many species specifically associated with periodontal disease, such as *Porphyromonas gingivalis*, *Tannerella forsythia*, and *Treponema denticola*, were not detected in any sites tested. In addition, the bacterial flora commonly thought to be involved in dental caries and deep - dental cavities, represented by *Streptococcus mutans*, *Lactobacillus species*, *Bifidobacterium species* and *Atopobium species*, were not detected in supra and sub gingival plaques from clinically healthy teeth. The bacterial species associated with sore throat such as lancifield group A  $\beta$ -haemolytic *Streptococcus pyogenes* were also not detected. It is necessary to first define the

bacterial flora of the healthy oral cavity before we can determine the role of oral bacteria n disease.

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